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☐ 1: P32628. UV excision repai...[gi:418413]

BLink, Domains, Links

LOCUS P32628 398 aa linear PLN 15-SEP-2003
 DEFINITION UV excision repair protein RAD23.
 ACCESSION P32628
 VERSION P32628 GI:418413
 DBSOURCE swissprot: locus RA23_YEAST, accession P32628;
 class: standard.
 created: Oct 1, 1993.
 sequence updated: Oct 1, 1993.
 annotation updated: Sep 15, 2003.
 xrefs: gi: 409246, gi: 409247, gi: 347494, gi: 347495, gi: 347496,
 gi: 347499, gi: 430831, gi: 4261672, gi: 430823, gi: 430824, gi:
 603625, gi: 603642, gi: 1077107
 xrefs (non-sequence databases): HSSPP54725, SGDS0000763,
 GOGO:0000111, GOGO:0000108, GOGO:0003684, InterProIPR004806,
 InterProIPR006636, InterProIPR000449, InterProIPR000626,
 PfamPF00627, PfamPF00240, SMARTSM00727, SMARTSM00165, SMARTSM00213,
 TIGRFAMsTIGR00601, PROSITEPS50030, PROSITEPS50053
 KEYWORDS DNA damage; DNA repair; Nuclear protein; Repeat.
 SOURCE Saccharomyces cerevisiae (baker's yeast)
 ORGANISM Saccharomyces cerevisiae
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 REFERENCE 1 (residues 1 to 398)
 AUTHORS Watkins,J.F., Sung,P., Prakash,L. and Prakash,S.
 TITLE The Saccharomyces cerevisiae DNA repair gene RAD23 encodes a
 nuclear protein containing a ubiquitin-like domain required for
 biological function
 JOURNAL Mol. Cell. Biol. 13 (12), 7757-7765 (1993)
 MEDLINE 94067136
 PUBMED 8246991
 REMARK SEQUENCE FROM N.A.
 REFERENCE 2 (residues 1 to 398)
 AUTHORS Melnick,L. and Sherman,F.
 TITLE The gene clusters ARC and COR on chromosomes 5 and 10,
 respectively, of Saccharomyces cerevisiae share a common ancestry
 JOURNAL J. Mol. Biol. 233 (3), 372-388 (1993)
 MEDLINE 94016558
 PUBMED 8411151
 REMARK SEQUENCE FROM N.A.
 STRAIN=B-6441
 REFERENCE 3 (residues 1 to 398)
 AUTHORS Dietrich,F.S., Mulligan,J.T., Hennessy,K.M., Yelton,M.A., Allen,E.,
 Araujo,R., Aviles,E., Berno,A., Brennan,T., Carpenter,J., Chen,E.,
 Cherry,J.M., Chung,E., Duncan,M., Guzman,E., Hartzell,G.,
 Hunicke-Smith,S., Hyman,R.W., Kayser,A., Komp,C., Lashkari,D.,
 Lew,H., Lin,D., Mosedale,D., Nakahara,K., Namath,A., Norgren,R.,
 Oefner,P., Oh,C., Petel,F.X., Roberts,D., Sehl,P., Schramm,S.,

TITLE Shogren,T., Smith,V., Taylor,P., Wei,Y., Botstein,D. and Davis,R.W.
JOURNAL The nucleotide sequence of *Saccharomyces cerevisiae* chromosome V
MEDLINE Nature 387 (6632 Suppl), 78-81 (1997)
PUBMED 97313264
REMARK 9169868
SEQUENCE FROM N.A.
STRAIN=S288c / AB972

COMMENT

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. The original entry is available from <http://www.expasy.ch/sprot> and <http://www.ebi.ac.uk/sprot>

[SUBCELLULAR LOCATION] Nuclear (Probable).
[SIMILARITY] Contains 1 ubiquitin-like domain.
[SIMILARITY] Contains 2 UBA domains.

FEATURES

	Location/Qualifiers
source	1..398 /organism="Saccharomyces cerevisiae" /db_xref="taxon:4932"
gene	1..398 /gene="RAD23" /note="synonyms: YEL037C, SYGP-ORF29"
Protein	1..398 /gene="RAD23" /product="UV excision repair protein RAD23"
Region	1..77 /gene="RAD23" /region_name="Domain" /note="UBIQUITIN-LIKE."
Region	146..186 /gene="RAD23" /region_name="Domain" /note="UBA 1."
Region	277 /gene="RAD23" /region_name="Conflict" /note="A -> R (IN REF. 2)."
Region	355..395 /gene="RAD23" /region_name="Domain" /note="UBA 2."

ORIGIN

1 mvsltfknfk kekvpldlep sntiletktk laqsiscees qikliysgkv lqdsktvsec
61 glkdgdqvfv mvsqkkstkt kvteppiape sattpgrens teaspsdas aapaatapeg
121 sqpqqeqtat tertesastp gfvvgterne tierimemgy qreeveralr aafnnpdrav
181 eyllmgipen lrqpepqqt aaaaepqsta attaeqpaed dlfaqaagg nassgalgtt
241 ggatdaaagg ppgsigltve dllslrqvvs gnpealapll enisarypql rehimanpev
301 fvsmlleavg dnmqdvmege dnmvegedie vtgeaaaagl gqgegegsfq vdytpeddqa
361 isrlcelgfe rdlviqvyfa cdkneeeaan ilfsdhad

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